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Cotton cultivar UA222

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(54) **COTTON CULTIVAR UA222**

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(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

A cotton cultivar, designated UA222, is disclosed. The invention relates to the seeds of cotton cultivar UA222, to the plants of cotton UA222 and to methods for producing a cotton plant produced by crossing the cultivar UA222 with itself or another cotton variety. The invention further relates to hybrid cotton seeds and plants produced by crossing the cultivar UA222 with another cotton cultivar.

23 Claims, No Drawings

COTTON CULTIVAR UA222

BACKGROUND OF THE INVENTION

The present invention relates to a cotton (*Gossypium*) seed, a cotton plant, a cotton cultivar, and a cotton hybrid. This invention further relates to a method for producing cotton seed and plants. All publications cited in this application are herein incorporated by reference.

Cotton is a soft, fluffy staple fiber that grows in a boll, or protective capsule, around the seeds of cotton plants of the genus *Gossypium*. The fiber is almost pure cellulose. The botanical purpose of cotton fiber is to aid in seed dispersal.

Cotton fiber most often is spun into yarn or thread and used to make a soft, breathable textile. The use of cotton for fabric is known to date to prehistoric times; fragments of cotton fabric dated from 5000 BC have been excavated in Mexico and Pakistan. Although cultivated since antiquity, it was the invention of the cotton gin that so lowered the cost of production that led to its widespread use, and it is the most widely used natural fiber cloth in clothing today.

There are four commercially-grown species of cotton, including *Gossypium hirsutum*, also known as upland cotton, which makes up 90% of the world production of cotton. Current estimates for world production are about 25 million tons annually, accounting for 2.5% of the world's arable land. China is the world's largest producer of cotton, but most of this is used domestically. The United States has been the largest exporter for many years.

There are numerous steps in the development of any novel, desirable plant germplasm. Plant breeding begins with the analysis and definition of problems and weaknesses of the current germplasm, the establishment of program goals, and the definition of specific breeding objectives. The next step is selection of germplasm that possess the traits to meet the program goals. The goal is to combine in a single cultivar an improved combination of desirable traits from the parental germplasm. In cotton, the important traits include higher fiber (lint) yield, earlier maturity, improved fiber quality, resistance to diseases and insects, resistance to drought and heat, and improved agronomic traits.

Choice of breeding or selection methods depends on the mode of plant reproduction, the heritability of the trait(s) being improved, and the type of cultivar used commercially (e.g., F_1 hybrid cultivar, pureline cultivar, etc.). For highly heritable traits, a choice of superior individual plants evaluated at a single location will be effective, whereas for traits with low heritability, selection should be based on mean values obtained from replicated evaluations of families of related plants. Popular selection methods commonly include pedigree selection, modified pedigree selection, mass selection, and recurrent selection.

The complexity of inheritance influences choice of the breeding method. Backcross breeding is used to transfer one or a few favorable genes for a highly heritable trait into a desirable cultivar. This approach has been used extensively for breeding disease-resistant cultivars. Various recurrent selection techniques are used to improve quantitatively inherited traits controlled by numerous genes. The use of recurrent selection in self-pollinating crops depends on the ease of pollination, the frequency of successful hybrids from each pollination, and the number of hybrid offspring from each successful cross.

Each breeding program should include a periodic, objective evaluation of the efficiency of the breeding procedure. Evaluation criteria vary depending on the goal and objectives, but should include gain from selection per year based on

comparisons to an appropriate standard, overall value of the advanced breeding lines, and number of successful cultivars produced per unit of input (e.g., per year, per dollar expended, etc.).

Promising advanced breeding lines are thoroughly tested and compared to popular cultivars in environments representative of the commercial target area(s) for three or more years. The best lines having superiority over the popular cultivars are candidates to become new commercial cultivars. Those lines still deficient in a few traits are discarded or utilized as parents to produce new populations for further selection.

These processes, which lead to the final step of marketing and distribution, usually take from seven to twelve years from the time the first cross is made. Therefore, development of new cultivars is a time-consuming process that requires precise forward planning, efficient use of resources, and a minimum of changes in direction.

A most difficult task is the identification of individuals that are genetically superior because for most traits the true genotypic value is masked by other confounding plant traits or environmental factors. One method of identifying a superior plant is to observe its performance relative to other experimental lines and widely grown standard cultivars. For many traits a single observation is inconclusive, and replicated observations over time and space are required to provide a good estimate of a line's genetic worth.

The goal of a commercial cotton breeding program is to develop new, unique, and superior cotton cultivars. The breeder initially selects and crosses two or more parental lines, followed by generation advancement and selection, thus producing many new genetic combinations. The breeder can theoretically generate billions of different genetic combinations via this procedure. The breeder has no direct control over which genetic combinations will arise in the limited population size which is grown. Therefore, two breeders will never develop the same line having the same traits.

Each year, the plant breeder selects the germplasm to advance to the next generation. This germplasm is grown under unique and different geographical, climatic, and soil conditions, and further selections are then made, during and at the end of the growing season. The lines which are developed are unpredictable. This unpredictability is because the breeder's selection occurs in unique environments, with no control at the DNA level (using conventional breeding procedures), and with millions of different possible genetic combinations being generated. A breeder of ordinary skill in the art cannot predict the final resulting lines he develops, except possibly in a very gross and general fashion. The same breeder cannot produce, with any reasonable likelihood, the same cultivar twice by using the exact same original parents and the same selection techniques. This unpredictability results in the expenditure of large amounts of research monies to develop superior new cotton cultivars.

Pureline cultivars of cotton are commonly bred by hybridization of two or more parents followed by selection. The complexity of inheritance, the breeding objectives, and the available resources influence the breeding method. Pedigree breeding, recurrent selection breeding, and backcross breeding are breeding methods commonly used in self pollinated crops such as cotton. These methods refer to the manner in which breeding pools or populations are made in order to combine desirable traits from two or more cultivars or various broad-based sources. The procedures commonly used for selection of desirable individuals or populations of individuals are called mass selection, plant-to-row selection, and single seed descent or modified single seed descent. One, or a

combination of these selection methods can be used in the development of a cultivar from a breeding population.

Pedigree breeding is primarily used to combine favorable genes into a totally new cultivar that is different in many traits than either parent used in the original cross. It is commonly used for the improvement of self-pollinating crops. Two parents which possess favorable, complementary traits are crossed to produce an F_1 (filial generation 1). An F_2 population is produced by selfing F_1 plants. Selection of desirable individual plants may begin as early as the F_2 generation wherein maximum gene segregation occurs. Individual plant selection can occur for one or more generations. Successively, seed from each selected plant can be planted in individual, identified rows or hills, known as progeny rows or progeny hills, to evaluate the line and to increase the seed quantity, or to further select individual plants. Once a progeny row or progeny hill is selected as having desirable traits, it becomes what is known as a breeding line that is specifically identifiable from other breeding lines that were derived from the same original population. At an advanced generation (i.e., F_3 or higher) seed of individual lines are evaluated in replicated testing. At an advanced stage the best lines or a mixture of phenotypically similar lines from the same original cross are tested for potential release as new cultivars.

The single seed descent procedure in the strict sense refers to planting a segregating population, harvesting one seed from every plant, and combining these seeds into a bulk which is planted the next generation. When the population has been advanced to the desired level of inbreeding, the plants from which lines are derived will each trace to different F_2 individuals. Primary advantages of the seed descent procedures are to delay selection until a high level of homozygosity (e.g., lack of gene segregation) is achieved in individual plants, and to move through these early generations quickly, usually through using winter nurseries.

The modified single seed descent procedures involve harvesting multiple seed (i.e., a single lock or a simple boll) from each plant in a population and combining them to form a bulk. Part of the bulk is used to plant the next generation and part is put in reserve. This procedure has been used to save labor at harvest and to maintain adequate seed quantities of the population.

Selection for desirable traits can occur at any segregating generation (F_2 and above). Selection pressure is exerted on a population by growing the population in an environment where the desired trait is maximally expressed and the individuals or lines possessing the trait can be identified. For instance, selection can occur for disease resistance when the plants or lines are grown in natural or artificially-induced disease environments, and the breeder selects only those individuals having little or no disease and are thus assumed to be resistant.

In addition to phenotypic observations, the genotype of a plant can also be examined. There are many laboratory-based techniques available for the analysis, comparison, and characterization of plant genotype. Among these are Isozyme Electrophoresis, Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length polymorphisms (AFLPs), Simple Sequence Repeats (SSRs—which are also referred to as Microsatellites), and Single Nucleotide Polymorphisms (SNPs).

Isozyme Electrophoresis and RFLPs have been widely used to determine genetic composition. Shoemaker and

Olsen, (Molecular Linkage Map of Soybean (*Glycine max* L. Merr.) pp. 6.131-6.138 in S. J. O'Brien (Ed.) *Genetic Maps: Locus Maps of Complex Genomes*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1993)) developed a molecular genetic linkage map that consisted of 25 linkage groups with about 365 RFLP, 11 RAPD, three classical markers, and four isozyme loci. See also, Shoemaker, R. C., RFLP Map of Soybean, pp. 299-309, in Phillips, R. L. and Vasil, I. K. (Eds.), *DNA-Based Markers in Plants*, Kluwer Academic Press, Dordrecht, the Netherlands (1994).

SSR technology is currently the most efficient and practical marker technology; more marker loci can be routinely used and more alleles per marker locus can be found using SSRs in comparison to RFLPs. For example, Diwan and Cregan described a highly polymorphic microsatellite locus in soybean with as many as 26 alleles. Diwan, N. and Cregan, P. B., *Theor. Appl. Genet.*, 95:22-225 (1997). SNPs may also be used to identify the unique genetic composition of the invention and progeny varieties retaining that unique genetic composition. Various molecular marker techniques may be used in combination to enhance overall resolution.

Molecular markers, which includes markers identified through the use of techniques such as Isozyme Electrophoresis, RFLPs, RAPDs, AP-PCR, DAF, SCARs, AFLPs, SSRs, and SNPs, may be used in plant breeding. One use of molecular markers is Quantitative Trait Loci (QTL) mapping. QTL mapping is the use of markers which are known to be closely linked to alleles that have measurable effects on a quantitative trait. Selection in the breeding process is based upon the accumulation of markers linked to the positive effecting alleles and/or the elimination of the markers linked to the negative effecting alleles from the plant's genome.

Molecular markers can also be used during the breeding process for the selection of qualitative traits. For example, markers closely linked to alleles or markers containing sequences within the actual alleles of interest can be used to select plants that contain the alleles of interest during a backcrossing breeding program. For example, molecular markers are used in soybean breeding for selection of the trait of resistance to soybean cyst nematode, see U.S. Pat. No. 6,162,967. The markers can also be used to select toward the genome of the recurrent parent and against the markers of the donor parent. Using this procedure can attempt to minimize the amount of genome from the donor parent that remains in the selected plants. It can also be used to reduce the number of crosses back to the recurrent parent needed in a backcrossing program. The use of molecular markers in the selection process is often called Genetic Marker Enhanced Selection. Molecular markers may also be used to identify and exclude certain sources of germplasm as parental varieties or ancestors of a plant by providing a means of tracking genetic profiles through crosses as discussed more fully hereinafter.

Mutation breeding is another method of introducing new traits into cotton varieties. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation (such as X-rays, Gamma rays, neutrons, Beta radiation, or ultraviolet radiation), chemical mutagens (such as base analogues like 5-bromo-uracil), antibiotics, alkylating agents (such as sulfur mustard, nitrogen mustards, epoxides, ethyleneamines, sulfates, sulfonates, sulfones, or lactones), azide, hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis the trait may then be incorporated into existing germ-

plasm by traditional breeding techniques. Details of mutation breeding can be found in *Principles of Cultivar Development* by Fehr, Macmillan Publishing Company (1993).

The production of double haploids can also be used for the development of homozygous varieties in a breeding program. Double haploids are produced by the doubling of a set of chromosomes from a heterozygous plant to produce a completely homozygous individual. For example, see Wan, et al., *Theor. Appl. Genet.*, 77:889-892 (1989).

Descriptions of other breeding methods that are commonly used for different traits and crops can be found in one of several reference books (e.g., Allard (1960); Simmonds (1979); Sneep, et al. (1979); Fehr (1987)).

Proper testing should detect any major faults and establish the level of superiority or improvement over current cultivars. In addition to showing superior performance, there must be a demand for a new cultivar that is compatible with industry standards or which creates a new market. The introduction of a new cultivar will incur additional costs to the seed producer, and to the grower, processor, and consumer, for special advertising, marketing and commercial production practices, and new product utilization. The testing preceding the release of a new cultivar should take into consideration research and development costs as well as technical superiority of the final cultivar. For seed-propagated cultivars, it must be feasible to produce seed easily and economically.

Cotton, including *Gossypium hirsutum* (Acala) and *Gossypium barbadense* (Pima), is an important and valuable field crop. Thus, a continuing goal of cotton plant breeders is to develop stable, high yielding cotton cultivars of both cotton species that are agronomically sound. The reasons for this goal are obviously to maximize the amount and quality of the fiber produced on the land used and to supply fiber, oil, and food for animals and humans. To accomplish this goal, the cotton breeder must select and develop plants that have the traits that result in superior cultivars.

The development of new cotton cultivars requires the evaluation and selection of parents and the crossing of these parents. The lack of predictable success of a given cross requires that a breeder, in any given year, make several crosses with the same or different breeding objectives.

The cotton flower is monoecious in that the male and female structures are in the same flower. The crossed or hybrid seed is produced by manual crosses between selected parents. Floral buds of the parent that is to be the female are emasculated prior to the opening of the flower by manual removal of the male anthers. At flowering, the pollen from flowers of the parent plants designated as male, are manually placed on the stigma of the previous emasculated flower. Seed developed from the cross is known as first generation (F_1) hybrid seed. Planting of this seed produces F_1 hybrid plants of which half their genetic component is from the female parent and half from the male parent. Segregation of genes begins at meiosis thus producing second generation (F_2) seed. Assuming multiple genetic differences between the original parents, each F_2 seed has a unique combination of genes.

The foregoing examples of the related art and limitations related therewith are intended to be illustrative and not exclusive. Other limitations of the related art will become apparent to those of skill in the art upon a reading of the specification.

SUMMARY OF THE INVENTION

The following embodiments and aspects thereof are described in conjunction with systems, tools, and methods which are meant to be exemplary and illustrative, not limiting in scope. In various embodiments, one or more of the above-

described problems have been reduced or eliminated, while other embodiments are directed to other improvements.

The present invention relates to a cotton seed, a cotton plant, a cotton cultivar, and a method for producing a cotton plant.

The present invention further relates to a method of producing cotton seeds and plants by crossing a plant of the instant invention with another cotton plant.

One aspect of the present invention relates to seed of the cotton variety UA222. The invention also relates to plants produced by growing the seed of the cotton variety UA222, as well as the derivatives of such plants. As used herein, the term "plant" includes plant cells, plant protoplasts, plant cells of a tissue culture from which cotton plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants, such as pollen, flowers, seeds, bolls, leaves, stems, and the like.

Another aspect of the invention relates to a tissue culture of regenerable cells of the cotton variety UA222, as well as plants regenerated therefrom, wherein the regenerated cotton plant expresses all the physiological and morphological characteristics of a plant grown from the cotton seed designated UA222.

Yet another aspect of the current invention is a cotton plant of the cotton variety UA222 comprising at least a first transgene, wherein the cotton plant is otherwise capable of expressing all the physiological and morphological characteristics of the cotton variety UA222. In particular embodiments of the invention, a plant is provided that comprises a single locus conversion. A single locus conversion may comprise a transgenic gene which has been introduced by genetic transformation into the cotton variety UA222 or a progenitor thereof. A transgenic or non-transgenic single locus conversion can also be introduced by backcrossing, as is well known in the art. In certain embodiments of the invention, the single locus conversion may comprise a dominant or recessive allele. The locus conversion may confer potentially any desired trait upon the plant as described herein.

Still yet another aspect of the invention relates to a first generation (F_1) hybrid cotton seed produced by crossing a plant of the cotton variety UA222 to a second cotton plant. Also included in the invention are the F_1 hybrid cotton plants grown from the hybrid seed produced by crossing the cotton variety UA222 to a second cotton plant. Still further included in the invention are the seeds of an F_1 hybrid plant produced with the cotton variety UA222 as one parent, the second generation (F_2) hybrid cotton plant grown from the seed of the F_1 hybrid plant, and the seeds of the F_2 hybrid plant.

Still yet another aspect of the invention is a method of producing cotton seeds comprising crossing a plant of the cotton variety UA222 to any second cotton plant, including itself or another plant of the variety UA222. In particular embodiments of the invention, the method of crossing comprises the steps of: (a) planting seeds of the cotton variety UA222; (b) cultivating cotton plants resulting from said seeds until said plants bear flowers; (c) allowing fertilization of the flowers of said plants; and (d) harvesting seeds produced from said plants.

Still yet another aspect of the invention is a method of producing hybrid cotton seeds comprising crossing the cotton variety UA222 to a second, distinct cotton plant which is nonisogenic to the cotton variety UA222. In particular embodiments of the invention, the crossing comprises the steps of: (a) planting seeds of cotton variety UA222 and a second, distinct cotton plant; (b) cultivating the cotton plants grown from the seeds until the plants bear flowers; (c) cross

pollinating a flower on one of the two plants with the pollen of the other plant; and (d) harvesting the seeds resulting from the cross pollinating.

Still yet another aspect of the invention is a method for developing a cotton plant in a cotton breeding program comprising: (a) obtaining a cotton plant, or its parts, of the variety UA222; and (b) employing said plant or parts as a source of breeding material using plant breeding techniques. In the method, the plant breeding techniques may be selected from the group consisting of recurrent selection, mass selection, bulk selection, backcrossing, pedigree breeding, genetic marker-assisted selection, and genetic transformation. In certain embodiments of the invention, the cotton plant of variety UA222 is used as the male or female parent.

Still yet another aspect of the invention is a method of producing a cotton plant derived from the cotton variety UA222, the method comprising the steps of: (a) preparing a progeny plant derived from cotton variety UA222 by crossing a plant of the cotton variety UA222 with a second cotton plant; and (b) crossing the progeny plant with itself or a second plant to produce a progeny plant of a subsequent generation which is derived from a plant of the cotton variety UA222. In one embodiment of the invention, the method further comprises: (c) crossing the progeny plant of a subsequent generation with itself or a second plant; and (d) repeating steps (b) and (c) for at least 2-10 additional generations to produce an inbred cotton plant derived from the cotton variety UA222. Also provided by the invention is a plant produced by this and the other methods of the invention. Plant variety UA222-derived plants produced by this and the other methods of the invention described herein may, in certain embodiments of the invention, be further defined as comprising the traits of plant variety UA222 given in Table 1.

In another aspect, the present invention provides regenerable cells for use in tissue culture of cotton plant UA222. The tissue culture will preferably be capable of regenerating plants having the physiological and morphological characteristics of the foregoing cotton plant, and of regenerating plants having substantially the same genotype as the foregoing cotton plant. Preferably, the regenerable cells in such tissue cultures will be embryos, protoplasts, meristematic cells, callus, pollen, leaves, anthers, pistils, roots, root tips, flowers, seeds, or stems. Still further, the present invention provides cotton plants regenerated from the tissue cultures of the invention.

The use of the word “a” or “an” when used in conjunction with the term “comprising” in the claims and/or the specification may mean “one,” but it is also consistent with the meaning of “one or more,” “at least one,” and “one or more than one.”

Other objects, features, and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

In addition to the exemplary aspects and embodiments described above, further aspects and embodiments will become apparent by study of the following descriptions.

DETAILED DESCRIPTION OF THE INVENTION

In the description and tables which follow, a number of terms are used. In order to provide a clear and consistent

understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided:

Allele. Allele is any of one or more alternative forms of a gene, all of which relate to one trait or characteristic. In a diploid cell or organism, the two alleles of a given gene occupy corresponding loci on a pair of homologous chromosomes.

Backcrossing. Backcrossing is a process in which a breeder repeatedly crosses hybrid progeny back to one of the parents, for example, a first generation hybrid F_1 with one of the parental genotypes of the F_1 hybrid.

Boll. The seed-bearing capsule of certain plants, especially cotton and flax.

Disease Resistance. As used herein, the term “disease resistance” is defined as the ability of plants to restrict the activities of a specified pest, such as an insect, fungus, virus, or bacterial.

Disease Tolerance. As used herein, the term “disease tolerance” is defined as the ability of plants to endure a specified pest (such as an insect, fungus, virus or bacteria) or an adverse environmental condition and still perform and produce in spite of this disorder.

Essentially all of the physiological and morphological characteristics. Essentially all of the physiological and morphological characteristics means a plant having essentially all of the physiological and morphological characteristics of the recurrent parent, except for the characteristics derived from the converted trait.

Elongation (E1). As used herein, the term “elongation” is defined as the measure of elasticity of a bundle of fibers as measured by HVI.

Length. As used herein, the term “length” is defined as 2.5% span length in inches of fiber as measured by High Volume Instrumentation (HVI).

Fiber Strength (T1). As used herein, the term “strength” is defined as the force required to break a bundle of fibers as measured in grams per millitex on the HVI.

Fruiting Nodes. As used herein, the term “fruiting nodes” is defined as the number of nodes on the main stem from which arise branches which bear fruit or bolls.

Gin Turnout. As used herein, the term “gin turnout” is defined as a fraction of lint in a machine harvested sample of seed cotton (lint, seed, and trash).

HVI. High Volume Instrumentation is a quality determination system used for cotton. Considered the standard USDA classing system.

Lint/Boll. As used herein, the term “lint/boll” is the weight of lint per boll.

Lint Index. As used herein, the term “lint index” refers to the weight of lint per seed in milligrams.

Lint Percent. As used herein, the term “lint percent” is defined as the lint (fiber) fraction of seed cotton (lint and seed). Also known as lint turnout.

Lint Yield. As used herein, the term “lint yield” is defined as the measure of the quantity of fiber produced on a given unit of land. Presented below in pounds of lint per acre.

Maturity. As used herein, the term “maturity” is defined as the HVI machine rating which refers to the degree of development of thickening of the fiber cell wall relative to the perimeter or effective diameter of the fiber.

Maturity Rating. As used herein, the term “maturity rating” is defined as a visual rating near harvest on the amount of opened bolls on the plant.

Micronaire. As used herein, the term “micronaire” is defined as a measure of the fineness of the fiber. Within a cotton cultivar, micronaire is also a measure of maturity.

Micronaire differences are governed by changes in perimeter or in cell wall thickness, or by changes in both. Within a cultivar, cotton perimeter is fairly constant and maturity will cause a change in micronaire. Consequently, micronaire has a high correlation with maturity within a variety of cotton. Maturity is the degree of development of cell wall thickness. Micronaire may not have a good correlation with maturity between varieties of cotton having different fiber perimeter. Micronaire values range from about 2.0 to 6.0:

Below 2.9	Very fine	Possible small perimeter but mature (good fiber), or large perimeter but immature (bad fiber).
2.9 to 3.7	Fine	Various degrees of maturity and/or perimeter.
3.8 to 4.6	Average	Average degree of maturity and/or perimeter.
4.7 to 5.5	Coarse	Usually fully-developed (mature), but larger perimeter.
5.6+	Very coarse	Fully-developed, large-perimeter fiber.

Plant Height. As used herein, the term “plant height” is defined as the average height in inches or centimeters of a group of plants.

Seed/boll. As used herein, the term “seed/boll” refers to the number of seeds per boll.

Seedcotton/boll. As used herein, the term “seedcotton/boll” refers to the weight of seedcotton per boll.

Single Trait Converted (Conversion). Single trait converted (conversion) plant refers to plants which are developed by a plant breeding technique called backcrossing or via genetic engineering wherein essentially all of the desired morphological and physiological characteristics of a variety are recovered in addition to the single trait transferred into the variety via the backcrossing technique or via genetic engineering.

Vegetative Nodes. As used herein, the term “vegetative nodes” is defined as the number of nodes from the cotyledonary node to the first fruiting branch on the main stem of the plant.

Cotton cultivar UA222 is a *Gossypium hirsutum* cotton variety. UA222 is a closed canopy (normal leaf) variety with hairy leaves and stems. Since hairy leaf cottons tend to have higher bract density than smooth leaf cottons, the marginal bract density for UA222 was relatively low considering its leaf pubescence rating. Lower values for marginal bract trichomes should contribute to less trash in ginned lint.

UA222 was derived from a cross between Arkot 9111 and STX8M007 made at the Northeast Research and Extension Center (Keiser, Ark.) in 2002, and was developed as part of an ongoing effort to develop improved cotton lines having enhanced yield, yield components, earliness, host plant resistance, and fiber properties. The F₁ population was increased at the USDA/ARS Tecoman Cotton Winter Breeding Nursery (Tecoman, Mexico). The F₂ and F₃ populations were seeded and thinned to uniform plant densities at Keiser in 2003 and 2004, respectively. In both years, bulk selections of bolls were made from visually superior individual plants after bacterial blight susceptible and morphological off-type plants were removed. Individual plants were selected from the F₄ generation, which were grown at Keiser in 2005. Seeds from these selections were evaluated as progeny rows at Keiser and Judd Hill in 2006 and as advanced progenies at Keiser, Marianna, and Rohwer in 2007.

In most tests, UA222 has produced lint yields greater than DP 393 (PVP 200400266), a well-adapted conventional variety, and its lint percentage was higher than SG105. These data suggest that UA222 is well-adapted to both clay and silt loam soils. UA222 displays high resistance to bacterial blight and is

similar to DP 393 in its response to most other diseases and to tarnished plant bug. The fiber quality of UA222 is very good; in most tests, it produced longer fiber length, higher length uniformity, lower micronaire, and higher elongation than DP 393 or SG 105 (PVP 9900190). UA222 displays an unusual combination of high yielding ability, favorable yield components, host plant resistance, early maturity and high fiber quality.

The cultivar has shown uniformity and stability, as described in the following Variety Description Information. It has been self-pollinated a sufficient number of generations with careful attention to uniformity of plant type. The cultivar has been increased with continued observation to uniformity.

Cotton cultivar UA222 has the following morphologic and other characteristics from data taken in Arkansas in September of 2011.

TABLE 1

VARIETY DESCRIPTION INFORMATION

Species:	<i>Gossypium hirsutum</i> L.
General:	
Plant Habit:	Intermediate
Foliage:	Intermediate
Stem Lodging:	Erect
Fruiting Branch:	Normal
Growth:	Intermediate
Leaf Color:	Medium green
Boll Shape:	Length is greater than width
Boll Breadth:	Broadest at base
Maturity (Date of 50% open bolls):	Approximately 125 days after planting
Plant:	
Cm to 1st Fruiting Branch (from cotyledonary node):	13.7
No. of Nodes to 1st Fruiting Branch (excluding cotyledonary node):	7.6
Mature Plant Height (from cotyledonary node to terminal):	104.0 cm
Leaf (Upper-most, fully expanded leaf):	
Type:	Normal
Pubescence:	Normal, hairy
Nectaries:	Present
Stem Pubescence:	Intermediate
Glands:	
Leaf:	Normal
Stem:	Normal
Calyx Lobe:	Absent
Flower:	
Petals (color):	Cream
Pollen (color):	Cream
Petal Spot:	Absent
Seed:	
Seed Index:	11.0 g
Lint Index:	7.7 g
Boll:	
Lint Percent (picked):	40.4
Number of Seeds per Boll:	25
Grams Seed Cotton per Boll:	4.8
Number of Locules per Boll:	4.0
Boll Type:	Open
Fiber Properties:	
Method (HVI or other):	HVI
Length (inches, 2.5% SL):	1.23
Uniformity (%):	85.2
Strength, T1 (g/tex):	31.9

TABLE 1-continued

VARIETY DESCRIPTION INFORMATION	
Elongation, E1 (%):	10.2
Micronaire:	4.4
Nematodes, Insects, and Pests:	
Bacterial Blight (Race 1):	Highly resistant
Bacterial Blight (Race 2):	Highly resistant
Bacterial Blight (Race 18):	Highly resistant
<i>Fusarium</i> Wilt:	Resistant
<i>Verticillium</i> Wilt:	Tolerant
Root-Knot Nematode:	Moderately tolerant
Tarnished Plant Bug (<i>Lygus lineolaris</i>):	Moderate resistance

This invention is also directed to methods for producing a cotton plant by crossing a first parent cotton plant with a second parent cotton plant, wherein the first or second cotton plant is the cotton plant from the cultivar UA222. Further, both the first and second parent cotton plants may be the cultivar UA222 (e.g., self-pollination). Therefore, any methods using the cultivar UA222 are part of this invention: selfing, backcrosses, hybrid breeding, and crosses to populations. Any plants produced using cultivar UA222 as parents are within the scope of this invention. As used herein, the term "plant" includes plant cells, plant protoplasts, plant cells of tissue culture from which cotton plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants, such as pollen, flowers, embryos, ovules, seeds, leaves, stems, roots, anthers, pistils, and the like. Thus, another aspect of this invention is to provide for cells which upon growth and differentiation produce a cultivar having essentially all of the physiological and morphological characteristics of UA222.

The present invention contemplates a cotton plant regenerated from a tissue culture of a cultivar (e.g., UA222) or hybrid plant of the present invention. As is well known in the art, tissue culture of cotton can be used for the in vitro regeneration of a cotton plant. Tissue culture of various tissues of cotton and regeneration of plants there from is well known and widely published.

FURTHER EMBODIMENTS OF THE INVENTION

With the advent of molecular biological techniques that have allowed the isolation and characterization of genes that encode specific protein products, scientists in the field of plant biology developed a strong interest in engineering the genome of plants to contain and express foreign genes, or additional, or modified versions of native, or endogenous, genes (perhaps driven by different promoters) in order to alter the traits of a plant in a specific manner. Such foreign additional and/or modified genes are referred to herein collectively as "transgenes." Over the last fifteen to twenty years several methods for producing transgenic plants have been developed, and the present invention, in particular embodiments, also relates to transformed versions of the claimed cultivar.

Plant transformation involves the construction of an expression vector which will function in plant cells. Such a vector comprises DNA comprising a gene under control of or operatively linked to a regulatory element (for example, a promoter). The expression vector may contain one or more such operably linked gene/regulatory element combinations. The vector(s) may be in the form of a plasmid, and can be used alone or in combination with other plasmids, to provide transformed cotton plants, using transformation methods as

described below to incorporate transgenes into the genetic material of the cotton plant(s).

Expression Vectors for Cotton Transformation: Marker Genes

Expression vectors include at least one genetic marker operably linked to a regulatory element (for example, a promoter) that allows transformed cells containing the marker to be either recovered by negative selection (i.e., inhibiting growth of cells that do not contain the selectable marker gene), or by positive selection (i.e., screening for the product encoded by the genetic marker). Many commonly used selectable marker genes for plant transformation are well known in the transformation arts, and include, for example, genes that code for enzymes that metabolically detoxify a selective chemical agent which may be an antibiotic or an herbicide, or genes that encode an altered target which is insensitive to the inhibitor. A few positive selection methods are also known in the art.

One commonly used selectable marker gene for plant transformation is the neomycin phosphotransferase II (nptII), which, when under the control of plant regulatory signals, confers resistance to kanamycin. Fraley, et al., *PNAS*, 80:4803 (1983). Another commonly used selectable marker gene is the hygromycin phosphotransferase gene which confers resistance to the antibiotic hygromycin. Vanden Elzen, et al., *Plant Mol. Biol.*, 5:299 (1985).

Additional selectable marker genes of bacterial origin that confer resistance to antibiotics include gentamycin acetyl transferase, streptomycin phosphotransferase, and aminoglycoside-3'-adenyl transferase, the bleomycin resistance determinant. Hayford, et al., *Plant Physiol.*, 86:1216 (1988); Jones, et al., *Mol. Gen. Genet.*, 210:86 (1987); Svab, et al., *Plant Mol. Biol.*, 14:197 (1990); Hille, et al., *Plant Mol. Biol.*, 7:171 (1986). Other selectable marker genes confer resistance to herbicides such as glyphosate, glufosinate, or bromoxynil. Comai, et al., *Nature*, 317:741-744 (1985); Gordon-Kamm, et al., *Plant Cell*, 2:603-618 (1990); and Stalker, et al., *Science*, 242:419-423 (1988).

Other selectable marker genes for plant transformation that are not of bacterial origin include, for example, mouse dihydrofolate reductase, plant 5-enolpyruvyl-shikimate-3-phosphate synthase and plant acetolactate synthase. Eichholtz, et al., *Somatic Cell Mol. Genet.*, 13:67 (1987); Shah, et al., *Science*, 233:478 (1986); Charest, et al., *Plant Cell Rep.*, 8:643 (1990).

Another class of marker genes for plant transformation requires screening of presumptively transformed plant cells rather than direct genetic selection of transformed cells for resistance to a toxic substance such as an antibiotic. These genes are particularly useful to quantify or visualize the spatial pattern of expression of a gene in specific tissues and are frequently referred to as reporter genes because they can be fused to a gene or gene regulatory sequence for the investigation of gene expression. Commonly used genes for screening presumptively transformed cells include β -glucuronidase (GUS), β -galactosidase, luciferase, and chloramphenicol acetyltransferase. Jefferson, R. A., *Plant Mol. Biol. Rep.*, 5:387 (1987); Teeri, et al., *EMBO J.*, 8:343 (1989); Koncz, et al., *PNAS*, 84:131 (1987); DeBlock, et al., *EMBO J.*, 3:1681 (1984).

In vivo methods for visualizing GUS activity that do not require destruction of plant tissue are available. Molecular Probes Publication 2908, IMAGENE GREEN, pp. 1-4 (1993) and Naleway, et al., *J. Cell Biol.*, 115:151a (1991). However, these in vivo methods for visualizing GUS activity have not proven useful for recovery of transformed cells because of

low sensitivity, high fluorescent backgrounds, and limitations associated with the use of luciferase genes as selectable markers.

More recently, a gene encoding Green Fluorescent Protein (GFP) has been utilized as a marker for gene expression in prokaryotic and eukaryotic cells. Chalfie, et al., *Science*, 263: 802 (1994). GFP and mutants of GFP may be used as screenable markers.

Expression Vectors for Cotton Transformation: Promoters

Genes included in expression vectors must be driven by a nucleotide sequence comprising a regulatory element (for example, a promoter). Several types of promoters are now well known in the transformation arts, as are other regulatory elements that can be used alone or in combination with promoters.

As used herein, "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, seeds, fibers, xylem vessels, tracheids, or sclerenchyma. Such promoters are referred to as "tissue-preferred." Promoters which initiate transcription only in certain tissue are referred to as "tissue-specific." A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue-specific, tissue-preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most environmental conditions.

A. Inducible Promoters:

An inducible promoter is operably linked to a gene for expression in cotton. Optionally, the inducible promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton. With an inducible promoter the rate of transcription increases in response to an inducing agent.

Any inducible promoter can be used in the instant invention. See Ward, et al., *Plant Mol. Biol.*, 22:361-366 (1993). Exemplary inducible promoters include, but are not limited to, that from the ACEI system which responds to copper (Mett, et al., *PNAS*, 90:4567-4571 (1993)); In2 gene from maize which responds to benzenesulfonamide herbicide safeners (Hershey, et al., *Mol. Gen. Genet.*, 227:229-237 (1991) and Gatz, et al., *Mol. Gen. Genet.*, 243:32-38 (1994)); or Tet repressor from Tn10 (Gatz, et al., *Mol. Gen. Genet.*, 227:229-237 (1991)). A particularly preferred inducible promoter is a promoter that responds to an inducing agent to which plants do not normally respond. An exemplary inducible promoter is the inducible promoter from a steroid hormone gene, the transcriptional activity of which is induced by a glucocorticosteroid hormone (Schena, et al., *PNAS*, 88:0421 (1991)).

B. Constitutive Promoters:

A constitutive promoter is operably linked to a gene for expression in cotton or the constitutive promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton.

Many different constitutive promoters can be utilized in the instant invention. Exemplary constitutive promoters include, but are not limited to, the promoters from plant viruses such as

the 35S promoter from CaMV (Odell, et al., *Nature*, 313:810-812 (1985)) and the promoters from such genes as rice actin (McElroy, et al., *Plant Cell*, 2:163-171 (1990)); ubiquitin (Christensen, et al., *Plant Mol. Biol.*, 12:619-632 (1989) and Christensen, et al., *Plant Mol. Biol.*, 18:675-689 (1992)); pEMU (Last, et al., *Theor. Appl. Genet.*, 81:581-588 (1991)); MAS (Velten, et al., *EMBO J.*, 3:2723-2730 (1984)); and maize H3 histone (Lepetit, et al., *Mol. Gen. Genet.*, 231:276-285 (1992) and Atanassova, et al., *Plant Journal*, 2 (3): 291-300 (1992)).

The ALS promoter, Xba1/NcoI fragment 5' to the *Brassica napus* ALS3 structural gene (or a nucleotide sequence similarity to said Xba1/NcoI fragment), represents a particularly useful constitutive promoter. See PCT Application No. WO 96/30530.

C. Tissue-Specific or Tissue-Preferred Promoters:

A tissue-specific promoter is operably linked to a gene for expression in cotton. Optionally, the tissue-specific promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton. Plants transformed with a gene of interest operably linked to a tissue-specific promoter produce the protein product of the transgene exclusively, or preferentially, in a specific tissue.

Any tissue-specific or tissue-preferred promoter can be utilized in the instant invention. Exemplary tissue-specific or tissue-preferred promoters include, but are not limited to, a root-preferred promoter, such as that from the phaseolin gene (Murai, et al., *Science*, 23:476-482 (1983) and Sengupta-Gopalan, et al., *PNAS*, 82:3320-3324 (1985)); a leaf-specific and light-induced promoter, such as that from cab or rubisco (Simpson, et al., *EMBO J.*, 4(11):2723-2729 (1985) and Timko, et al., *Nature*, 318:579-582 (1985)); an anther-specific promoter, such as that from LAT52 (Twell, et al., *Mol. Gen. Genet.*, 217:240-245 (1989)); a pollen-specific promoter, such as that from Zm13 (Guerrero, et al., *Mol. Gen. Genet.*, 244:161-168 (1993)); or a microspore-preferred promoter, such as that from apg (Twell, et al., *Sex. Plant Reprod.*, 6:217-224 (1993)).

Signal Sequences for Targeting Proteins to Subcellular Compartments

Transport of protein produced by transgenes to a subcellular compartment, such as the chloroplast, vacuole, peroxisome, glyoxysome, cell wall, or mitochondrion, or for secretion into the apoplast, is accomplished by means of operably linking the nucleotide sequence encoding a signal sequence to the 5' and/or 3' region of a gene encoding the protein of interest. Targeting sequences at the 5' and/or 3' end of the structural gene may determine, during protein synthesis and processing, where the encoded protein is ultimately compartmentalized.

The presence of a signal sequence directs a polypeptide to either an intracellular organelle or subcellular compartment or for secretion to the apoplast. Many signal sequences are known in the art. See, for example, Becker, et al., *Plant Mol. Biol.*, 20:49 (1992); Close, P. S., Master's Thesis, Iowa State University (1993); Knox, C., et al., *Plant Mol. Biol.*, 9:3-17 (1987); Lerner, et al., *Plant Physiol.*, 91:124-129 (1989); Fontes, et al., *Plant Cell*, 3:483-496 (1991); Matsuoka, et al., *PNAS*, 88:834 (1991); Gould, et al., *J. Cell. Biol.*, 108:1657 (1989); Creissen, et al., *Plant J.*, 2:129 (1991); Kalderon, et al., *Cell*, 39:499-509 (1984); Steifel, et al., *Plant Cell*, 2:785-793 (1990).

Foreign Protein Genes and Agronomic Genes

With transgenic plants according to the present invention, a foreign protein can be produced in commercial quantities. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants which are harvested in a conventional manner, and a foreign protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr, *Anal. Biochem.*, 114:92-6 (1981).

According to a preferred embodiment, the transgenic plant provided for commercial production of foreign protein is a cotton plant. In another preferred embodiment, the biomass of interest is seed. For the relatively small number of transgenic plants that show higher levels of expression, a genetic map can be generated, primarily via conventional RFLP, PCR, and SSR analysis, which identifies the approximate chromosomal location of the integrated DNA molecule. For exemplary methodologies in this regard, see Glick and Thompson, *Methods in Plant Molecular Biology and Biotechnology*, CRC Press, Boca Raton, 269:284 (1993). Map information concerning chromosomal location is useful for proprietary protection of a subject transgenic plant. If unauthorized propagation is undertaken and crosses made with other germplasm, the map of the integration region can be compared to similar maps for suspect plants, to determine if the latter have a common parentage with the subject plant. Map comparisons would involve hybridizations, RFLP, PCR, SSR and sequencing, all of which are conventional techniques.

Likewise, by means of the present invention, agronomic genes can be expressed in transformed plants. More particularly, plants can be genetically engineered to express various phenotypes of agronomic interest. Exemplary genes implicated in this regard include, but are not limited to, those categorized below:

A. Genes That Confer Resistance to Pests or Disease and That Encode:

1. Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example, Jones, et al., *Science*, 266:789 (1994) (cloning of the tomato Cf-9 gene for resistance to *Cladosporium fulvum*); Martin, et al., *Science*, 262:1432 (1993) (tomato Pto gene for resistance to *Pseudomonas syringae* pv. tomato encodes a protein kinase); Mindrinos, et al., *Cell*, 78:1089 (1994) (Arabidopsis RSP2 gene for resistance to *Pseudomonas syringae*).

2. A gene conferring resistance to a pest, such as nematodes. See, e.g., PCT Application No. WO 96/30517; PCT Application No. WO 93/19181.

3. A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser, et al., *Gene*, 48:109 (1986), who disclose the cloning and nucleotide sequence of a Bt δ -endotoxin gene. Moreover, DNA molecules encoding δ -endotoxin genes can be purchased from American Type Culture Collection, Manassas, Va., for example, under ATCC Accession Nos. 40098, 67136, 31995, and 31998.

4. A lectin. See, for example, the disclosure by Van Damme, et al., *Plant Molec. Biol.*, 24:25 (1994), who disclose the nucleotide sequences of several *Clivia miniata* mannose-binding lectin genes.

5. A vitamin-binding protein such as avidin. See PCT Application No. US 93/06487. The application teaches the use of avidin and avidin homologues as larvicides against insect pests.

6. An enzyme inhibitor, for example, a protease or proteinase inhibitor or an amylase inhibitor. See, for example, Abe, et al., *J. Biol. Chem.*, 262:16793 (1987) (nucleotide sequence of rice cysteine proteinase inhibitor); Huub, et al., *Plant Molec. Biol.*, 21:985 (1993) (nucleotide sequence of cDNA encoding tobacco proteinase inhibitor I); Sumitani, et al., *Biosci. Biotech. Biochem.*, 57:1243 (1993) (nucleotide sequence of *Streptomyces nitrosporeus* α -amylase inhibitor); and U.S. Pat. No. 5,494,813 (Hepher and Atkinson, issued Feb. 27, 1996).

7. An insect-specific hormone or pheromone, such as an ecdysteroid and juvenile hormone, a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof. See, for example, the disclosure by Hammock, et al., *Nature*, 344:458 (1990), of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone.

8. An insect-specific peptide or neuropeptide which, upon expression, disrupts the physiology of the affected pest. For example, see the disclosures of Regan, *J. Biol. Chem.*, 269:9 (1994) (expression cloning yields DNA coding for insect diuretic hormone receptor) and Pratt, et al., *Biochem. Biophys. Res. Comm.*, 163:1243 (1989) (an allostatin is identified in *Diptera punctata*). See also, U.S. Pat. No. 5,266,317 to Tomalski, et al., who disclose genes encoding insect-specific, paralytic neurotoxins.

9. An insect-specific venom produced in nature by a snake, a wasp, etc. For example, see Pang, et al., *Gene*, 116:165 (1992), for disclosure of heterologous expression in plants of a gene coding for a scorpion insectotoxic peptide.

10. An enzyme responsible for a hyper-accumulation of a monoterpene, a sesquiterpene, a steroid, a hydroxamic acid, a phenylpropanoid derivative, or another non-protein molecule with insecticidal activity.

11. An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule. For example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase, and a glucanase, whether natural or synthetic. See PCT Application No. WO 93/02197 in the name of Scott, et al., which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also, Kramer, et al., *Insect Biochem. Molec. Biol.*, 23:691 (1993), who teach the nucleotide sequence of a cDNA encoding tobacco hornworm chitinase, and Kawalleck, et al., *Plant Molec. Biol.*, 21:673 (1993), who provide the nucleotide sequence of the parsley ubi4-2 polyubiquitin gene.

12. A molecule that stimulates signal transduction. For example, see the disclosure by Botella, et al., *Plant Molec. Biol.*, 24:757 (1994), of nucleotide sequences for mung bean calmodulin cDNA clones and Griess, et al., *Plant Physiol.*, 104:1467 (1994), who provide the nucleotide sequence of a maize calmodulin cDNA clone.

13. A hydrophobic moment peptide. See PCT Application No. WO 95/16776 (disclosure of peptide derivatives of Tachyplesin which inhibit fungal plant pathogens) and PCT Application No. WO 95/18855 (teaches synthetic antimicrobial peptides that confer disease resistance).

14. A membrane permease, a channel former or a channel blocker. For example, see the disclosure of Jaynes, et al., *Plant Sci.*, 89:43 (1993), of heterologous expression of a

cecropin-13 lytic peptide analog to render transgenic tobacco plants resistant to *Pseudomonas solanacearum*.

15. A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. See, Beachy, et al., *Ann. Rev. Phytopathol.*, 28:451 (1990). Coat protein-mediated resistance has been conferred upon transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. Id.

16. An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected enzyme, killing the insect. See, Taylor, et al., *Abstract #497*, Seventh Int'l Symposium on Molecular Plant-Microbe Interactions (Edinburgh, Scotland) (1994) (enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments).

17. A virus-specific antibody. See, for example, Tavlaroraki, et al., *Nature*, 366:469 (1993), who show that transgenic plants expressing recombinant antibody genes are protected from virus attack.

18. A developmental-arrestive protein produced in nature by a pathogen or a parasite. Thus, fungal endo- α -1,4-D-polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo- α -1,4-D-galacturonase. See, Lamb, et al., *Bio/technology*, 10:1436 (1992). The cloning and characterization of a gene which encodes a bean endopolygalacturonase-inhibiting protein is described by Toubart, et al., *Plant J.*, 2:367 (1992).

19. A developmental-arrestive protein produced in nature by a plant. For example, Logemann, et al., *Bio/technology*, 10:305 (1992), have shown that transgenic plants expressing the barley ribosome-inactivating gene have an increased resistance to fungal disease.

B. Genes That Confer Resistance to an Herbicide:

1. An herbicide that inhibits the growing point or meristem, such as an imidazolinone or a sulfonylurea. Exemplary genes in this category code for mutant ALS and AHAS enzyme as described, for example, by Lee, et al., *EMBO J.*, 7:1241 (1988), and Miki, et al., *Theor. Appl. Genet.*, 80:449 (1990), respectively.

2. Glyphosate (resistance conferred by mutant 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) and aroA genes, respectively) and other phosphono compounds such as glufosinate (phosphinothricin acetyl transferase (PAT) and *Streptomyces hygroscopicus* PAT bar genes), and pyridinoyl or phenoxy propionic acids and cyclohexones (ACCase inhibitor-encoding genes). See, for example, U.S. Pat. No. 4,940,835 to Shah, et al., which discloses the nucleotide sequence of a form of EPSP which can confer glyphosate resistance. A DNA molecule encoding a mutant aroA gene can be obtained under ATCC Accession No. 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Pat. No. 4,769,061 to Comai. European Patent Application No. 0 333 033 to Kumada, et al., and U.S. Pat. No. 4,975,374 to Goodman, et al., disclose nucleotide sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a PAT gene is provided in European Application No. 0 242 246 to Leemans, et al. DeGreef, et al., *Bio/technology*, 7:61 (1989), describe the production of transgenic plants that express chimeric bar genes coding for PAT activity. Exemplary of genes conferring resistance to phenoxy propionic

acids and cyclohexones, such as sethoxydim and haloxyfop are the Acc1-S1, Acc1-S2, and Acc1-S3 genes described by Marshall, et al., *Theor. Appl. Genet.*, 83:435 (1992).

3. An herbicide that inhibits photosynthesis, such as a triazine (psbA and gs+ genes) or a benzonitrile (nitrilase gene). Przibila, et al., *Plant Cell*, 3:169 (1991), describe the transformation of *Chlamydomonas* with plasmids encoding mutant psbA genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Pat. No. 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441, and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes, et al., *Biochem. J.*, 285:173 (1992).

C. Genes That Confer or Contribute to a Value-Added Trait, such as:

1. Modified fatty acid metabolism, for example, by transforming a plant with an antisense gene of stearyl-ACP desaturase to increase stearic acid content of the plant. See Knutzon, et al., *PNAS*, 89:2624 (1992).

2. Decreased phytate content: (a) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. See, for example, Van Hartingsveldt, et al., *Gene*, 127:87 (1993), for a disclosure of the nucleotide sequence of an *Aspergillus niger* phytase gene; and (b) A gene could be introduced that reduced phytate content. For example, in maize, this could be accomplished by cloning and then reintroducing DNA associated with the single allele which is responsible for maize mutants characterized by low levels of phytic acid. See, Raboy, et al., *Maydica*, 35:383 (1990).

3. Modified carbohydrate composition effected, for example, by transforming plants with a gene coding for an enzyme that alters the branching pattern of starch. See, Shiroza, et al., *J. Bacteriol.*, 170:810 (1988) (nucleotide sequence of *Streptococcus* mutants fructosyltransferase gene); Steinmetz, et al., *Mol. Gen. Genet.*, 20:220 (1985) (nucleotide sequence of *Bacillus subtilis* levansucrase gene); Pen, et al., *Bio/technology*, 10:292 (1992) (production of transgenic plants that express *Bacillus licheniformis* α -amylase); Elliot, et al., *Plant Molec. Biol.*, 21:515 (1993) (nucleotide sequences of tomato invertase genes); Sogaard, et al., *J. Biol. Chem.*, 268:22480 (1993) (site-directed mutagenesis of barley α -amylase gene); and Fisher, et al., *Plant Physiol.*, 102:1045 (1993) (maize endosperm starch branching enzyme II). Methods for Cotton Transformation

Numerous methods for plant transformation have been developed, including biological and physical, plant transformation protocols. See, for example, Miki, et al., "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick and Thompson (Eds.), CRC Press, Inc., Boca Raton, pp. 67-88 (1993). In addition, expression vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber, et al., "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology*, Glick and Thompson (Eds.), CRC Press, Inc., Boca Raton, pp. 89-119 (1993).

A. *Agrobacterium*-Mediated Transformation:

One method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium*. See, for example, Horsch, et al., *Science*, 227:1229 (1985). *A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria which genetically transform plant cells. The Ti and Ri plasmids of *A. tumefaciens* and *A. rhizogenes*, respectively, carry genes responsible for genetic transformation of the plant. See, for example, Kado, C. I., *Crit. Rev. Plant Sci.*, 10:1 (1991). Descriptions of *Agrobacterium*

vector systems and methods for *Agrobacterium*-mediated gene transfer are provided by Gruber, et al., supra, Miki, et al., supra, and Moloney, et al., *Plant Cell Rep.*, 8:238 (1989). See also, U.S. Pat. No. 5,563,055 (Townsend and Thomas), issued Oct. 8, 1996.

B. Direct Gene Transfer:

Several methods of plant transformation, collectively referred to as direct gene transfer, have been developed as an alternative to *Agrobacterium*-mediated transformation. A generally applicable method of plant transformation is microprojectile-mediated transformation wherein DNA is carried on the surface of microprojectiles measuring 1 μ m to 4 μ m. The expression vector is introduced into plant tissues with a biolistic device that accelerates the microprojectiles to speeds of 300 m/s to 600 m/s which is sufficient to penetrate plant cell walls and membranes. Sanford, et al., *Part. Sci. Technol.*, 5:27 (1987); Sanford, J. C., *Trends Biotech.*, 6:299 (1988); Klein, et al., *Bio/technology*, 6:559-563 (1988); Sanford, J. C., *Physiol Plant*, 7:206 (1990); Klein, et al., *Bio/technology*, 10:268 (1992). See also, U.S. Pat. No. 5,015,580 (Christou, et al.), issued May 14, 1991; U.S. Pat. No. 5,322,783 (Tomes, et al.), issued Jun. 21, 1994.

Another method for physical delivery of DNA to plants is sonication of target cells. Zhang, et al., *Bio/technology*, 9:996 (1991). Alternatively, liposome and spheroplast fusion have been used to introduce expression vectors into plants. Deshayes, et al., *EMBO J.*, 4:2731 (1985); Christou, et al., *PNAS*, 84:3962 (1987). Direct uptake of DNA into protoplasts using CaCl_2 precipitation, polyvinyl alcohol, or poly-L-ornithine has also been reported. Hain, et al., *Mol. Gen. Genet.*, 199:161 (1985) and Draper, et al., *Plant Cell Physiol.* 23:451 (1982). Electroporation of protoplasts and whole cells and tissues has also been described. Donn, et al., In Abstracts of VIIth International Congress on Plant Cell and Tissue Culture IAPTC, A2-38, p. 53 (1990); D'Halluin, et al., *Plant Cell*, 4:1495-1505 (1992); and Spencer, et al., *Plant Mol. Biol.*, 24:51-61 (1994).

Following transformation of cotton target tissues, expression of the above-described selectable marker genes allows for preferential selection of transformed cells, tissues, and/or plants, using regeneration and selection methods now well known in the art.

The foregoing methods for transformation would typically be used for producing a transgenic variety. The transgenic variety could then be crossed, with another (non-transformed or transformed) variety, in order to produce a new transgenic variety. Alternatively, a genetic trait which has been engineered into a particular cotton cultivar using the foregoing transformation techniques could be moved into another cultivar using traditional backcrossing techniques that are well known in the plant breeding arts. For example, a backcrossing approach could be used to move an engineered trait from a public, non-elite variety into an elite variety, or from a variety containing a foreign gene in its genome into a variety or varieties which do not contain that gene. As used herein, "crossing" can refer to a simple X by Y cross, or the process of backcrossing, depending on the context.

Single-Gene Conversion

When the term "cotton plant" is used in the context of the present invention, this also includes any single gene conversions of that variety. The term "single gene converted plant" as used herein refers to those cotton plants which are developed by a plant breeding technique called backcrossing wherein essentially all of the desired morphological and physiological characteristics of a variety are recovered in addition to the single gene transferred into the variety via the backcrossing technique. Backcrossing methods can be used

with the present invention to improve or introduce a characteristic into the variety. The term "backcrossing" as used herein refers to the repeated crossing of a hybrid progeny back to the recurrent parent, i.e., backcrossing 1, 2, 3, 4, 5, 6, 7, 8, 9, or more times to the recurrent parent. The parental cotton plant which contributes the gene for the desired characteristic is termed the "nonrecurrent" or "donor parent". This terminology refers to the fact that the nonrecurrent parent is used one time in the backcross protocol and therefore does not recur. The parental cotton plant to which the gene or genes from the nonrecurrent parent are transferred is known as the recurrent parent as it is used for several rounds in the backcrossing protocol (Poehlman & Sleper (1994); Fehr (1987)). In a typical backcross protocol, the original variety of interest (recurrent parent) is crossed to a second variety (nonrecurrent parent) that carries the single gene of interest to be transferred. The resulting progeny from this cross are then crossed again to the recurrent parent and the process is repeated until a cotton plant is obtained wherein essentially all of the desired morphological and physiological characteristics of the recurrent parent are recovered in the converted plant, in addition to the single transferred gene from the nonrecurrent parent, as determined at the 5% significance level when grown in the same environmental conditions.

The selection of a suitable recurrent parent is an important step for a successful backcrossing procedure. The goal of a backcross protocol is to alter or substitute a single trait or characteristic in the original variety. To accomplish this, a single gene of the recurrent variety is modified or substituted with the desired gene from the nonrecurrent parent, while retaining essentially all of the rest of the desired genetic, and therefore the desired physiological and morphological, constitution of the original variety. The choice of the particular nonrecurrent parent will depend on the purpose of the backcross. One of the major purposes is to add some commercially desirable, agronomically important trait to the plant. The exact backcrossing protocol will depend on the characteristic or trait being altered to determine an appropriate testing protocol. Although backcrossing methods are simplified when the characteristic being transferred is a dominant allele, a recessive allele may also be transferred. In this instance it may be necessary to introduce a test of the progeny to determine if the desired characteristic has been successfully transferred.

Many single gene traits have been identified that are not regularly selected for in the development of a new variety but that can be improved by backcrossing techniques. Single gene traits may or may not be transgenic. Examples of these traits include but are not limited to, male sterility, waxy starch, herbicide resistance, resistance for bacterial, fungal, or viral disease, insect resistance, male fertility, enhanced nutritional quality, industrial usage, yield stability, and yield enhancement. These genes are generally inherited through the nucleus. Several of these single gene traits are described in U.S. Pat. Nos. 5,959,185; 5,973,234; and 5,977,445, the disclosures of which are specifically hereby incorporated by reference.

Further reproduction of the variety can occur by tissue culture and regeneration. Tissue culture of various tissues of cotton and regeneration of plants therefrom is well known and widely published. For example, reference may be had to Komatsuda, T., et al., *Crop Sci.*, 31:333-337 (1991); Stephens, P. A., et al., *Theor. Appl. Genet.*, 82:633-635 (1991); Komatsuda, T., et al., *Plant Cell, Tissue and Organ Culture*, 28:103-113 (1992); Dhir, S., et al., *Plant Cell Rep.*, 11:285-289 (1992); Pandey, P., et al., *Japan J. Breed.*, 42:1-5 (1992); and Shetty, K., et al., *Plant Science*, 81:245-251 (1992); as well as U.S. Pat. No. 5,024,944 issued Jun. 18,

1991 to Collins, et al., and U.S. Pat. No. 5,008,200 issued Apr. 16, 1991 to Ranch, et al. Thus, another aspect of this invention is to provide cells which upon growth and differentiation produce cotton plants having the physiological and morphological characteristics of cotton cultivar UA222.

As used herein, the term "tissue culture" indicates a composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant. Exemplary types of tissue cultures are protoplasts, calli, plant clumps, and plant cells that can generate tissue culture that are intact in plants or parts of plants, such as embryos, pollen, flowers, seeds, leaves, stems, roots, root tips, anthers, pistils, and the like. Means for preparing and maintaining plant tissue culture are well known in the art. By way of example, a tissue culture comprising organs has been used to produce regenerated plants. U.S. Pat. Nos. 5,959,185; 5,973,234; and 5,977,445, described certain techniques.

This invention also is directed to methods for producing a cotton plant by crossing a first parent cotton plant with a second parent cotton plant wherein the first or second parent cotton plant is a cotton plant of the cultivar UA222. Further, both first and second parent cotton plants can come from the cotton cultivar UA222. Additionally, the first or second parent cotton plants can be either *Gossypium hirsutum* or *Gossypium barbadense*, or any other cotton plant. Thus, any such methods using the cotton cultivar UA222 are part of this invention: selfing, backcrosses, hybrid production, crosses to populations, and the like. All plants produced using cotton cultivar UA222 as a parent are within the scope of this invention, including those developed from varieties derived from cotton cultivar UA222. Advantageously, the cotton cultivar could be used in crosses with other, different, cotton plants to produce first generation (F_1) cotton hybrid seeds and plants with superior characteristics. The other, different, cotton plants may be *Gossypium hirsutum* or *Gossypium barbadense* or another cotton cultivar. The cultivar of the invention can also be used for transformation where exogenous genes are introduced and expressed by the cultivar of the invention. Genetic variants created either through traditional breeding methods using cultivar UA222 or through transformation of UA222 by any of a number of protocols known to those of skill in the art are intended to be within the scope of this invention.

The following describes breeding methods that may be used with cultivar UA222 in the development of further cotton plants. One such embodiment is a method for developing a UA222 progeny cotton plant in a cotton plant breeding program comprising: obtaining the cotton plant, or a part thereof, of cultivar UA222, utilizing said plant or plant part as a source of breeding material, and selecting a UA222 progeny plant with molecular markers in common with UA222 and/or with morphological and/or physiological characteristics selected from the characteristics listed in Table 1. Breeding steps that may be used in the cotton plant breeding program include pedigree breeding, backcrossing, mutation breeding, and recurrent selection. In conjunction with these steps, techniques such as RFLP-enhanced selection, genetic marker enhanced selection (for example, SSR markers), and the making of double haploids may be utilized.

Another method involves producing a population of cultivar UA222 progeny cotton plants, comprising crossing cultivar UA222 with another cotton plant, thereby producing a population of cotton plants, which, on average, derive 50% of their alleles from cultivar UA222. The other cotton plant may be *Gossypium hirsutum* or *Gossypium barbadense* or any other cotton plant. A plant of this population may be selected and repeatedly selfed or sibbed with a cotton cultivar resulting from these successive filial generations. One embodiment

of this invention is the cotton cultivar produced by this method and that has obtained at least 50% of its alleles from cultivar UA222.

One of ordinary skill in the art of plant breeding would know how to evaluate the traits of two plant varieties to determine if there is no significant difference between the two traits expressed by those varieties. For example, see Fehr and Walt, *Principles of Cultivar Development*, pp. 261-286 (1987). Thus the invention includes cotton cultivar UA222 progeny cotton plants comprising a combination of at least two UA222 traits selected from the group consisting of those listed in Table 1 or the UA222 combination of traits listed in the Summary of the Invention, so that said progeny cotton plant is not significantly different for said traits than cotton cultivar UA222 as determined at the 5% significance level when grown in the same environment. Using techniques described herein, molecular markers may be used to identify said progeny plant as a UA222 progeny plant. Mean trait values may be used to determine whether trait differences are significant, and preferably the traits are measured on plants grown under the same environmental conditions. Once such a variety is developed its value is substantial since it is important to advance the germplasm base as a whole in order to maintain or improve traits such as yield, disease resistance, pest resistance, and plant performance in extreme environmental conditions.

Progeny of cultivar UA222 may also be characterized through their filial relationship with cotton cultivar UA222, as for example, being within a certain number of breeding crosses of cotton cultivar UA222. A breeding cross is a cross made to introduce new genetics into the progeny, and is distinguished from a cross, such as a self or a sib cross, made to select among existing genetic alleles. The lower the number of breeding crosses in the pedigree, the closer the relationship between cotton cultivar UA222 and its progeny. For example, progeny produced by the methods described herein may be within 1, 2, 3, 4 or 5 breeding crosses of cotton cultivar UA222.

TABLES

UA222 was compared to DP 393 and SG 105 (PVP 9900190) in replicated field tests at four Arkansas Agricultural Experiment Station sites in 2008 through 2010, as shown in Tables 2-5. The test locations included the Northeast Research and Extension Center at Keiser on Sharkey clay (very-fine, smectitic, thermic Chromic Epiaquerts), the Judd Hill Cooperative Research Site at Judd Hill on Dundee silt loam (fine-silty, mixed, active, thermic Typic Endoaqualls), the Lon Mann Cotton Research Station at Marianna on Callaway silt loam (fine-silty, mixed, thermic Glossaquic Fragiudalfs), and the Southeast Branch Experiment Station at Rohwer on Hebert silt loam (fine-silty, mixed, active, thermic Aeric Epiaqualls).

Each field test was arranged in a randomized complete block design with four replications of two-row plots (12-14 m×1 m). Standard production practices with furrow irrigation were followed in each test. Percentage of open bolls was visually rated within 1-3 days before or after first application of defoliant to the plots. Seedcotton yields were determined by machine picking for all plots. Hand-harvested boll samples, collected from two of the four replications, were ginned on a laboratory gin. Variables determined using the gin data and samples included lint fraction, seed index, lint index, fibers per seed, seed per area, fiber density, and HVI (High Volume Instrument) fiber parameters. Fiber density, an estimate of the number of fibers per mm² seed surface area, was

determined using a regression equation to calculate seed surface area based on fuzzy seed weights (Groves and Bourland, 2010). Procedures for collecting and processing boll samples were the same as described for the Arkansas Cotton Variety Test (Bourland et al., 2011). The average lint percentage for an entry over two replications at each location was used to convert seedcotton yield to lint yield. All data were analyzed by SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.). Years and replications were considered to be random, while entry and location were fixed.

Leaves, stems, and bracts were sampled at the Keiser test site in 2008 through 2010. Leaf and stem pubescence were rated using the rating system established by Bourland et al. (2003). Bracts were sampled and marginal trichome density was determined using methods of Bourland and Hornbeck (2007). Leaf and bract data were analyzed by SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.) with years and replications being random and entries being fixed.

UA222 was also evaluated in the 2010 Regional Breeders' Testing Network (RBTN; www.cottonrbtn.com), which included agronomic field tests at 14 locations from Suffolk, Va. to Shafter, Calif.

Table 2 shows the lint yields in pounds per acre of UA222 compared to check cultivars (DP 393 and SG 105) at locations in the Mississippi River Delta region of Arkansas from 2008 through 2010. Locations are arranged from north (left) to south (right) in the table.

TABLE 2

2008-2010 Arkansas Strain Tests (lb/acre)				
Cultivar	Keiser	Judd Hill	Marianna	Rohwer
UA222	1151	1237	1142	976
DP 393	1022	1092	1083	935
SG 105	986	1168	985	893
LSD0.10	68	84	70	85

As shown in Table 2, compared to the check cultivars, the lint yields of UA222 were higher than the average of the two check cultivars at Keiser, Judd Hill and Marianna, and equal to the check cultivars at Rohwer.

Table 3 shows the yield and lint component-related parameters of UA222 compared to check cultivars in 2008-2010 at Arkansas test sites. Each parameter was determined in tests at Keiser, Judd Hill, Marianna, and Rohwer. Lint fraction, seed index, lint index and fibers per seed, and fiber density were determined from boll samples taken from two replications per test. Lint yield and seed per acre were determined on four replications per test. Location by line interaction was not significant ($P=0.10$) for any parameter.

TABLE 3

2008-2010 Arkansas Strain Tests							
Cultivar	Lint yield (lb/acre)	Seed/acre (no. $\times 10^6$)	Lint Index (g)	Seed index (g)	Lint Fraction (%)	Fibers/seed (no.)	Fiber density (no./mm ²)
UA222	1127	6.672	7.7	11.0	40.4	16657	154
DP 393	1033	6.416	7.3	10.6	40.3	15777	149
SG 105	1006	6.244	7.3	11.0	39.5	15342	142
LSD0.10	93	ns	0.4	0.4	0.8	690	6

As shown in Table 3, the lint yields of UA222 exceeded yields of each check cultivar. Together with Table 2, these data suggest that UA222 is well-adapted to both clay and silt loam soils. Compared to the check cultivars, UA222 derived

its higher yield from an increase in lint per seed (lint index) rather than seed per area. According to Lewis et al. (2000), increased reliance on high lint index relative to seeds produced per area should contribute to more stable yield production. The higher lint index and higher fibers per seed of UA222 may be partly attributed to its higher seed index. Fiber density and lint percentage of UA222 were higher than SG 105. The measurement of fiber density attempts to compensate for variation in seed size by estimating the number of fibers per unit area of seed surface area.

UA222 was also evaluated in the 2010 Regional Breeders' Testing Network (RBTN; www.cottonrbtn.com), which included agronomic field tests at 14 different U.S. locations. Among the 33 entries in the 2010 RBTN, UA222 produced the highest lint yield over all locations, and equaled the highest yielding entry at all locations except Suffolk (VA), St. Joseph (LA), College Station (TX), and Maricopa (AZ). These yields indicate that UA222 is broadly adapted to contrasting growing conditions.

Table 4 shows the morphological and host plant resistance traits for UA222 and check cultivars in the 2008-2010 Arkansas tests. The plant height and percentage of open bolls (visually estimated) measurements were taken at the approximate time of defoliation in each test. The location by line interaction was not significant ($P=0.10$). The leaf and stem pubescence was visually rated on 6 plants per plot for 4 repetitions at the Keiser, Ark. site from 1 (smooth) to 9 (pilose) using the rating system developed by Bourland et al. (2003). The number of marginal bract trichomes was determined on 6 plants per plot for 4 repetitions at the Keiser, Ark. site in 2008-2010 using methods described by Bourland and Hornbeck (2007). The percentages of flowers with discoloured anthers were determined in 12 repetitions of tests at the Keiser, Ark. site in 2009-2010, with all lines included in the same test each year. Discolored anthers were due to feeding by tarnished plant bugs, *Lygus lineolaris*, for which the susceptible check was a Frego-bract breeding line. The percentage of plants showing *Fusarium* wilt comes from evaluations at the 2010 National Cotton *Fusarium* Wilt Test in Tallahassee, Ala.; the susceptible check was 'Rowden' and the resistant check was M315.

Response to tarnished plant bug (*Lygus lineolaris*) was determined in small plot field tests conducted at Keiser, Ark., in 2009-2010. Single-row plots, 6 m \times 1 m, were replicated 12 times in a randomized complete block (RCB) design, and managed to encourage tarnished plant bug populations. Plots were sequentially examined for five to eight days (six flowers per plot per day) over a two-week period in August of each year. Damaged flowers, as indicated by discolored anthers, were enumerated. A collective measure of percentage of damaged flowers over the sequential samples was determined for each plot.

All pest resistance data collected in Arkansas, except bacterial blight data, were analyzed using SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.) with years and replications as random and entries being fixed.

TABLE 4

2008-2010 Arkansas Strain Tests							
Cultivar	Plant height (cm)	Open bolls (%)	Leaf pubescence (1-9)	Stem pubescence (1-9)	Bract trichomes (no./cm)	Damaged flowers (%)	<i>Fusarium</i> wilt (%)
UA222	104	53	4.3	5.8	34.7	36	4
DP 393	106	53	2.0	6.6	32.0	34	—
SG 105	103	57	2.4	5.8	29.5	43	—
Res. check	—	—	—	—	—	—	1
Sus. check	—	—	—	—	—	91	23
LSD0.05	3	2	0.5	0.7	2.7	5	4

As shown in Table 4, the maturity of UA222 is similar to DP 393 and slightly later than SG105 as indicated by its plant height and open boll percentage. Compared to DP 393, UA222 had higher trichome density on leaves, lower density on stems and equal density on bract margins. Based on these data, UA222 would be classified as having hairy leaves and stems. Since hairy leaf cottons tend to have higher bract density than smooth leaf cottons, the marginal bract density for UA222 was relatively low considering its leaf pubescence rating. Lower values for marginal bract trichomes should contribute to less trash in ginned lint. UA222 had percentages of wilted plants equal to the resistant check in response to *Fusarium* wilt in the 2010 National Cotton *Fusarium* Wilt Test. UA222 was more resistant to tarnished plant bug than SG105 in field tests conducted in 2009 and 2010. Additionally, UA222 is highly resistant to bacterial blight, tolerant to *Verticillium* wilt, and moderately tolerant to root-knot nematode.

Table 5 shows the fiber traits for UA222 compared to check cultivars in 2008-2010 at the Arkansas test sites. The fiber parameters were determined in tests at Keiser, Judd Hill, Marianna, and Rohwer. Location by line interaction was not significant ($P=0.10$) for any parameter. Fiber parameters were determined by HVI on lint from boll samples taken from two replications per test. The quality score (Q-score) is an index based on four fiber parameters (relative weight): fiber length (50%), micronaire (25%), uniformity (15%) and strength (10%).

TABLE 5

2008-2010 Arkansas Strain Tests						
Cultivar	Quality score	Micronaire	Fiber length (in.)	Uniformity index (%)	Fiber Strength (g/tex)	Fiber elongation (%)
UA222	75	4.38	1.23	85.2	31.9	10.2
DP 393	61	4.63	1.19	84.7	32.1	9.5
SG 105	54	4.81	1.17	84.0	30.3	9.2
LSD0.05	5	0.10	0.01	0.4	0.8	0.4

As shown in Table 5, the Q-score of UA222 greatly exceeded those of each check cultivar. Higher Q-scores for UA222 were associated with longer fiber length, higher length uniformity, and lower micronaire. The fiber strength of UA222 was equal to DP 393 and higher than SG 105, while its fiber elongation (not included in the Q-score) was higher than either check cultivar.

Relative variation among fiber traits for UA222, DP 393, and SG 105 across the 14 locations of the 2010 RBTN were similar to those found in the Arkansas tests.

The use of the terms “a,” “an,” and “the,” and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to

cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms “comprising,” “having,” “including,” and “containing” are to be construed as open-ended terms (i.e., meaning “including, but not limited to,”) unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. For example, if the range 10-15 is disclosed, then 11, 12, 13, and 14 are also disclosed. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., “such as”) provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

DEPOSIT INFORMATION

A deposit of the BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS proprietary COTTON CULTIVAR UA222 disclosed above and recited in the appended claims has been made with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Va. 20110. The date of deposit was Feb. 16, 2012. The deposit of 2,500 seeds was taken from the same deposit maintained by BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS since prior to the filing date of this application. All restrictions will be irrevocably removed upon granting of a patent, and the deposit is intended to meet all of the requirements of 37 C.F.R. §§1.801-1.809. The ATCC Accession Number is PTA-12548. The deposit will be maintained in the depository for a period of thirty years, or five years after the last request, or for the enforceable life of the patent, whichever is longer, and will be replaced as necessary during that period.

What is claimed is:

1. A seed of cotton cultivar UA222, wherein a representative sample of seed of said cultivar was deposited under ATCC Accession No. PTA-12548.

2. A cotton plant, or a regenerable part thereof, produced by growing the seed of claim 1.

3. A tissue culture of cells produced from the plant of claim 2, wherein said cells of the tissue culture are produced from a plant part selected from the group consisting of leaves, pollen, embryos, cotyledons, hypocotyl, meristematic cells, roots, root tips, pistils, anthers, flowers, and stems.

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4. A protoplast produced from the plant of claim 2.
5. A protoplast produced from the tissue culture of claim 3.
6. A cotton plant regenerated from the tissue culture of claim 3, wherein the plant has all of the morphological and physiological characteristics of cultivar UA222 listed in Table 1.
7. A method for producing F₁ hybrid cotton seed, wherein the method comprises crossing the plant of claim 2 with a different cotton plant and harvesting the resultant F₁ hybrid cotton seed.
8. A hybrid cotton seed produced by the method of claim 7.
9. A hybrid cotton plant, or a regenerable part thereof, produced by growing said hybrid seed of claim 8.
10. A method of producing an herbicide resistant cotton plant, wherein the method comprises transforming the cotton plant of claim 2 with a transgene, wherein the transgene confers resistance to an herbicide selected from the group consisting of imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.
11. An herbicide resistant cotton plant produced by the method of claim 10.
12. A method of producing an insect resistant cotton plant, wherein the method comprises transforming the cotton plant of claim 2 with a transgene that confers insect resistance.
13. An insect resistant cotton plant produced by the method of claim 12.
14. The cotton plant of claim 13, wherein the transgene encodes a *Bacillus thuringiensis* endotoxin.
15. A method of producing a disease resistant cotton plant, wherein the method comprises transforming the cotton plant of claim 2 with a transgene that confers disease resistance.
16. A disease resistant cotton plant produced by the method of claim 15.
17. A method of producing a cotton plant with modified fatty acid metabolism or modified carbohydrate metabolism, wherein the method comprises transforming the cotton plant of claim 2 with a transgene encoding a protein selected from the group consisting of phytase, fructosyltransferase, levansucrase, α -amylase, invertase and starch branching enzyme, or DNA encoding an antisense of stearyl-ACP desaturase.
18. A cotton plant having modified fatty acid metabolism or modified carbohydrate metabolism produced by the method of claim 17.

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19. A method of introducing a desired trait into cotton cultivar UA222, wherein the method comprises:
 - (a) crossing a UA222 plant, wherein a representative sample of seed was deposited under ATCC Accession No. PTA-12548, with a plant of another cotton cultivar that comprises a desired trait to produce progeny plants, wherein the desired trait is selected from the group consisting of male sterility, herbicide resistance, insect resistance, modified fatty acid metabolism, modified carbohydrate metabolism and resistance to bacterial disease, fungal disease or viral disease;
 - (b) selecting one or more progeny plants that have the desired trait;
 - (c) backcrossing the selected progeny plants with the UA222 plants to produce backcross progeny plants;
 - (d) selecting for backcross progeny plants that have the desired trait; and
 - (e) repeating steps (c) and (d) two or more times in succession to produce selected third or higher backcross progeny plants that comprise the desired trait.
20. A cotton plant produced by the method of claim 19, wherein the plant has the desired trait and otherwise all of the physiological and morphological characteristics of cotton cultivar UA222 listed in Table 1.
21. The cotton plant of claim 20, wherein the desired trait is herbicide resistance and the resistance is conferred to an herbicide selected from the group consisting of imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.
22. The cotton plant of claim 20, wherein the desired trait is insect resistance and the insect resistance is conferred by a transgene encoding a *Bacillus thuringiensis* endotoxin.
23. The cotton plant of claim 20, wherein the desired trait is modified fatty acid metabolism or modified carbohydrate metabolism and said desired trait is conferred by a nucleic acid encoding a protein selected from the group consisting of phytase, fructosyltransferase, levansucrase, α -amylase, invertase and starch branching enzyme, or DNA encoding an antisense of stearyl-ACP desaturase.

* * * * *